

0590  
08/15

# 4

OIPE

## RAW SEQUENCE LISTING

DATE: 08/17/2001

PATENT APPLICATION: US/09/866,248A

TIME: 14:23:44

Input Set : A:\57155A.txt

Output Set: N:\CRF3\08172001\I866248A.raw

5 <110> APPLICANT: Gerald, Christophe P.G.  
7 Jones, Kenneth A.  
9 Bonini, James A.  
11 Borowsky, Beth  
15 <120> TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors  
17 and Uses Thereof  
21 <130> FILE REFERENCE: 1795/57155-A  
C--> 25 <140> CURRENT APPLICATION NUMBER: US/09/866,248A  
C--> 27 <141> CURRENT FILING DATE: 2001-05-25  
31 <150> PRIOR APPLICATION NUMBER: 09/161,113  
33 <151> PRIOR FILING DATE: 1998-09-25  
37 <160> NUMBER OF SEQ ID NOS: 42  
41 <170> SOFTWARE: PatentIn Ver. 2.0 - beta  
45 <210> SEQ ID NO: 1  
47 <211> LENGTH: 1410  
49 <212> TYPE: DNA  
51 <213> ORGANISM: Rattus norvegicus  
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59 ggagcagaca gtatggaggc ggagccctcc cagcctccca acggcagctg gcccctgggt 120  
61 cagaacggga gtgatgtgga gaccagcatg gcaaccagcc tcaccttctc ctctactac 180  
63 caacactcct ctccggtggc agccatgttc atcgcgccct acgtgtctcat ctctctctc 240  
65 tgcattggtg gcaaacaccct ggtctgtctc attgtgtctc agaaccggca catgcgcact 300  
67 gtcaccaaca tgtttatcct caacctggcc gtcagcgacc tgctggtggg catcttctgc 360  
69 atgcccacaa cccttgtgga caaccttacc actggttggc cttttgacaa cgccacatgc 420  
71 aagatgagcg gcttgggtgca gggcatgtcc gtgtctgcat cggttttcac actggtggcc 480  
73 atcgctgtgg aaaggttccg ctgcatcggt caccctttcc gcgagaagct gaccttcgg 540  
75 aaggcgtgtg tcaccatcgc ggtgatctgg gctctggcgc tgctcatcat gtgtccctcg 600  
77 gcggtcactc tgacagtcac ccgagaggag catcaacttc tgctggatgc tcgtaaccgc 660  
79 tcttaccgcg tctactcggt ctgggaggcc tggcccgaga agggcatgcg caaggtctac 720  
81 accgcggtgc tcttcgcgca catctacctg gtgcccgtgg cgtctatcgt agtgatgtac 780  
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95 gcccaacaag aagcctactc ggagcgggcc aaccgcctcc tgcgcaggcg ggtggtggtg 1200  
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113 <213> ORGANISM: Rattus norvegicus  
117 <400> SEQUENCE: 2

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see page 5

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119 Met Glu Ala Glu Pro Ser Gln Pro Pro Asn Gly Ser Trp Pro Leu Gly
121   1           5           10           15
125 Gln Asn Gly Ser Asp Val Glu Thr Ser Met Ala Thr Ser Leu Thr Phe
127           20           25           30
131 Ser Ser Tyr Tyr Gln His Ser Ser Pro Val Ala Ala Met Phe Ile Ala
133           35           40           45
137 Ala Tyr Val Leu Ile Phe Leu Leu Cys Met Val Gly Asn Thr Leu Val
139           50           55           60
143 Cys Phe Ile Val Leu Lys Asn Arg His Met Arg Thr Val Thr Asn Met
145   65           70           75           80
149 Phe Ile Leu Asn Leu Ala Val Ser Asp Leu Leu Val Gly Ile Phe Cys
151           85           90           95
155 Met Pro Thr Thr Leu Val Asp Asn Leu Ile Thr Gly Trp Pro Phe Asp
157           100          105          110
161 Asn Ala Thr Cys Lys Met Ser Gly Leu Val Gln Gly Met Ser Val Ser
163           115          120          125
167 Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val Glu Arg Phe Arg Cys
169           130          135          140
173 Ile Val His Pro Phe Arg Glu Lys Leu Thr Leu Arg Lys Ala Leu Phe
175 145           150          155          160
179 Thr Ile Ala Val Ile Trp Ala Leu Ala Leu Leu Ile Met Cys Pro Ser
181           165          170          175
185 Ala Val Thr Leu Thr Val Thr Arg Glu Glu His His Phe Met Leu Asp
187           180          185          190
191 Ala Arg Asn Arg Ser Tyr Pro Leu Tyr Ser Cys Trp Glu Ala Trp Pro
193           195          200          205
197 Glu Lys Gly Met Arg Lys Val Tyr Thr Ala Val Leu Phe Ala His Ile
199           210          215          220
203 Tyr Leu Val Pro Leu Ala Leu Ile Val Val Met Tyr Val Arg Ile Ala
205 225           230          235          240
209 Arg Lys Leu Cys Gln Ala Pro Gly Pro Ala Arg Asp Thr Glu Glu Ala
211           245          250          255
215 Val Ala Glu Gly Arg Thr Ser Arg Arg Arg Ala Arg Val Val His
217           260          265          270
221 Met Leu Val Met Val Ala Leu Phe Phe Thr Leu Ser Trp Leu Pro Leu
223           275          280          285
227 Trp Val Leu Leu Leu Leu Ile Asp Tyr Gly Glu Leu Ser Glu Leu Gln
229           290          295          300
233 Leu His Leu Leu Ser Val Tyr Ala Phe Pro Leu Ala His Trp Leu Ala
235 305           310          315          320
239 Phe Phe His Ser Ser Ala Asn Pro Ile Ile Tyr Gly Tyr Phe Asn Glu
241           325          330          335
245 Asn Phe Arg Arg Gly Phe Gln Ala Ala Phe Arg Ala Gln Leu Cys Trp
247           340          345          350
251 Pro Pro Trp Ala Ala His Lys Gln Ala Tyr Ser Glu Arg Pro Asn Arg
253           355          360          365
257 Leu Leu Arg Arg Arg Val Val Val Asp Val Gln Pro Ser Asp Ser Gly
259           370          375          380
263 Leu Pro Ser Glu Ser Gly Pro Ser Ser Gly Val Pro Gly Pro Gly Arg

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265 385          390          395          400
269 Leu Pro Leu Arg Asn Gly Arg Val Ala His Gln Asp Gly Pro Gly Glu
271          405          410          415
275 Gly Pro Gly Cys Asn His Met Pro Leu Thr Ile Pro Ala Trp Asn Ile
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291 <211> LENGTH: 200
293 <212> TYPE: DNA
295 <213> ORGANISM: Homo sapiens
299 <400> SEQUENCE: 3
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303 gccaccccggt ctacaaacct caccttctcc tctactatc agcacacctc ccctgtggcg 120
305 gccatgttca ttgtggccta tgcgctcatc ttctgtctct gcatgggtgg caacaccctg 180
307 gtctgtttca tctgtctcaa                200
311 <210> SEQ ID NO: 4
313 <211> LENGTH: 66
315 <212> TYPE: PRT
317 <213> ORGANISM: Homo sapiens
321 <400> SEQUENCE: 4
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325 1          5          10          15
329 Thr Asn Thr Glu Ala Thr Pro Ala Thr Asn Leu Thr Phe Ser Ser Tyr
331          20          25          30
335 Tyr Gln His Thr Ser Pro Val Ala Ala Met Phe Ile Val Ala Tyr Ala
337          35          40          45
341 Leu Ile Phe Leu Leu Cys Met Val Gly Asn Thr Leu Val Cys Phe Ile
343          50          55          60
347 Val Leu
349 65
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357 <211> LENGTH: 1302
359 <212> TYPE: DNA
361 <213> ORGANISM: Homo sapiens
365 <400> SEQUENCE: 5
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369 gaaaactggc atcccatctg gaatgtcaat gacacaaagc atcatctgta ctacagatatt 120
371 aatattacct atgtgaacta ctatcttcac cagcctcaag tggcagcaat cttcattatt 180
373 tctacttttc tgatcttctt tttgtgcatg atgggaaata ctgtggtttg ctttattgta 240
375 atgaggaaca aacatatgca cacagtcact aatctcttca tcttaaacct ggccataagt 300
377 gatttactag ttggcatatt ctgcatgcct ataactgcg tggacaatat tatagcagga 360
379 tggccatttg gaaacacgat gtgcaagatc agtggattgg tccagggaat atctgtcgca 420
381 gcttcagttc ttacgttagt tgcaattgct gtagataggt tccagtgtgt ggtctacct 480
383 tttaaaccaa agctcactat caagacagcg tttgtcatta ttatgatcat ctgggtccta 540
385 gccatcacca ttatgtctcc atctgcagta atgttacatg tgcaagaaga aaaatattac 600
387 cgagtgcagc tcaactccca gaataaaacc agtccagtct actggtgccg ggaagactgg 660
389 ccaaatacagg aaatgaggaa gatctacacc actgtgctgt ttgccaacat ctacctggct 720
391 cccctctccc tcatgtgcat catgtatgga aggattggaa tttactctt cagggctgca 780
393 gttcctcaca caggcaggaa gaaccaggag cagtggcacg tgggtgccag gaagaagcag 840
395 aagatcatta agatgtctct gattgtggcc ctgcttttta ttctctcatg gctgccctg 900

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Output Set: N:\CRF3\08172001\I866248A.raw

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399 aacatctaca tctacccttt tgcacactgg ctggcattcg gcaacagcag tgtcaatccc 1020
401 atcatttatg gtttcttcaa cgagaatttc cgccgtgggt tccaagaagc tttccagctc 1080
403 cagctctgcc aaaaaagagc aaagcctatg gaagcttatg ccctaaaagc taaaagccat 1140
405 gtgctcataa acacatctaa tcagcttgct caggaatota catttcaaaa ccctcatggg 1200
407 gaaaccttgc tttataggaa aagtgtgtaa aaaccccaac aggaattagt gatggaagaa 1260
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431 Trp Asn Val Asn Asp Thr Lys His His Leu Tyr Ser Asp Ile Asn Ile
433 20 25 30
437 Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala Ala Ile Phe
439 35 40 45
443 Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys Met Met Gly Asn Thr
445 50 55 60
449 Val Val Cys Phe Ile Val Met Arg Asn Lys His Met His Thr Val Thr
451 65 70 75 80
455 Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu Val Gly Ile
457 85 90 95
461 Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala Gly Trp Pro
463 100 105 110
467 Phe Gly Asn Thr Met Cys Lys Ile Ser Gly Leu Val Gln Gly Ile Ser
469 115 120 125
473 Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val Asp Arg Phe
475 130 135 140
479 Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Ile Lys Thr Ala
481 145 150 155 160
485 Phe Val Ile Ile Met Ile Ile Trp Val Leu Ala Ile Thr Ile Met Ser
487 165 170 175
491 Pro Ser Ala Val Met Leu His Val Gln Glu Glu Lys Tyr Tyr Arg Val
493 180 185 190
497 Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val Tyr Trp Cys Arg Glu
499 195 200 205
503 Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr Thr Thr Val Leu Phe
505 210 215 220
509 Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile Met Tyr Gly
511 225 230 235 240
515 Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val Pro His Thr Gly Arg
517 245 250 255
521 Lys Asn Gln Glu Gln Trp His Val Val Ser Arg Lys Lys Gln Lys Ile
523 260 265 270
527 Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe Ile Leu Ser Trp Leu
529 275 280 285
533 Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Ala Asp Leu Ser Pro

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TIME: 14:23:44

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535      290      295      300
539 Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr Pro Phe Ala His Trp
541 305      310      315      320
545 Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile Ile Tyr Gly Phe Phe
547      325      330      335
551 Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala Phe Gln Leu Gln Leu
553      340      345      350
557 Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr Ala Leu Lys Ala Lys
559      355      360      365
563 Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu Val Gln Glu Ser Thr
565      370      375      380
569 Phe Gln Asn Pro His Gly Glu Thr Leu Leu Tyr Arg Lys Ser Ala Glu
571 385      390      395      400
575 Lys Pro Gln Gln Glu Leu Val Met Glu Glu Leu Lys Glu Thr Thr Asn
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595 <213> ORGANISM: Homo sapiens
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605 cctgtggcgg ccattgttcat tgtggcctat gcgctcatct tctgtctctg catggtgggc 180
607 aacaccctgg tctgtttcat cgtgctcaag aaccggcaca tgcatactgt caccaacatg 240
609 ttcctctcca acctggctgt cagtgcactg ctgggtggga tcttctgcat gccaccacc 300
611 cttgtggaca acctcatcac tgggtggccc ttcgacaatg ccacatgcaa gatgagcggc 360
613 ttggtgcagg gcatgtctgt gtcggcttcc gttttcacac tgggtggccat tgctgtggaa 420
615 aggttccgct gcatcgtgca ccttttccgc gagaagctga ccctgcggaa ggcgctcgtc 480
617 accatcgccg tcatctgggc cctggcgctg ctcatcatgt gtccctcggc cgtcacgctg 540
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621 tactcctgct gggaggcctg gcccgagaag ggcattgcga gggctctacac cactgtgctc 660
623 ttctcgaca tctacctggc gccgctggcg ctcatcgtgg tcatgtacgc ccgcatcgcg 720
625 cgcaagctct gccaggcccc gggcccgccc cccgggggcg aggaggctgc ggaccgcga 780
627 gcatcgcggc gcagagcgcg cgtggtgcac atgctggtca tgggtggcgt gttcttcacg 840
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631 ccgcagctgc acctggtcac cgtctacgcc tcccccttcg cgcactggct ggcttcttc 960
633 aacagcagcg ccaaccccat catctacggc tacttcaacg agaacttccg ccgcggcttc 1020
635 caggccgctt tccgcgccc cctctgccc cgcccgctcg ggagccacaa ggaggcctac 1080
637 tccgagcggc ccggcgggct tctgcacagg cgggtcttcg tgggtggtgc gccagcgac 1140
639 tccgggctgc cctctgagtc gggccctagc agtggggccc ccaggcccgg ccgcctccc 1200
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649 <211> LENGTH: 430
651 <212> TYPE: PRT
653 <213> ORGANISM: Homo sapiens
657 <400> SEQUENCE: 8

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 08/17/2001

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TIME: 14:23:45

Input Set : A:\57155A.txt

Output Set: N:\CRF3\08172001\I866248A.raw

L:25 M:270 C: Current Application Number differs, Replaced Application Number

L:27 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:847 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:875 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10